

XX Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE;
 PI Roberts NA, Roberts PC, Walther DM, Wolfe JL;
 XX WPI; 1997-043122/04.
 DR
 XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region -
 PT used in the treatment and detection of HCV infection, esp. hepatitis
 PT and Hepato-carcinoma
 XX
 PS Claim 1; Page 31; 100pp; English.
 XX
 CC The sequences given in AAT80211-382 represent synthetic oligonucleotides
 CC which are complementary to a portion of the 5' untranslated region (UTR)
 CC of hepatitis C virus (HCV). These sequences may be used in a
 CC pharmaceutical composition for the control or prevention of HCV
 CC infection. They may be used to inhibit replication or expression of
 CC HCV or for detecting the presence of HCV in a sample. They may be used
 CC to inhibit HCV replication in a cell and are therefore useful in the
 CC treatment of HCV infections such as chronic and acute hepatitis and
 CC hepatocarcinoma. This oligo was used in a luciferase assay to determine
 CC whether it binds successfully to its target.
 CC
 XX Sequence 12 BP; 1 A; 2 C; 7 G; 2 U; 0 other;
 SQ
 Query Match 100.0%; Score 12; DB 18; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GGGGUCGCGAG 12
 Db 1 999gucucgag 12
 Db
 RESULT 2
 AA23540/c
 ID AA23540 standard; DNA; 12 BP.
 XX
 AC AA23540;
 XX
 DT 21-DEC-1999 (first entry)
 XX
 DE HCV wild type genome probe.
 XX
 KW Assay; amplification; hybridisation; probe: detection; viral; bacterial;
 KW cellular; yeast; fungal; primer; ss.
 XX
 OS Synthetic.
 OS Hepatitis C virus.
 XX
 FN DE19814828-A1.
 XX
 PD 07-OCT-1999.
 XX
 PF 02-APR-1998; 98DE-1014828.
 XX
 PR 02-APR-1998; 98DE-1014828.
 XX
 PA (HOFF) ROCHE DIAGNOSTICS GMBH.
 XX
 PI Kessler C, Haberland G, Batz H, Oerum H;
 XX
 DR WPI; 1999-552286/47.
 XX
 PT Nucleic acid amplification assay for detecting viral, bacterial,
 PT cellular, yeast or fungal nucleic acids -
 XX
 PS Example 1; Page 21; 28pp; German.
 XX
 CC This invention describes a novel assay for a nucleic acid comprises:
 CC (a) generating amplification products from a fragment of the nucleic
 CC acid, (b) contacting the amplification products with a probe; and

CC (c) detecting hybridization between the amplification product and the
 CC probe. The assay is useful for detection of viral, bacterial, cellular,
 CC yeast or fungal nucleic acids in human, animal, bacterial, plant, yeast
 CC or fungal samples, e.g. feces, smears, cell suspensions, cultures or
 CC tissue, cell or liquid biopsy samples. This sequence represents a
 CC probe used in the method of the invention.
 XX
 SQ Sequence 12 BP; 2 A; 7 C; 2 G; 1 T; 0 other;
 Query Match 100.0%; Score 12; DB 20; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GGGGUCGCGAG 12
 Db 12 GGGGTCCTGAG 1
 Db
 RESULT 3
 AAX24037/c
 ID AAX24037 standard; DNA; 12 BP.
 XX
 AC AAX24037;
 XX
 DT 28-JUN-1999 (first entry)
 XX
 DE Ruthenium-labelled DNA probe.
 XX
 KW Amplification; medical; forensic; diagnosis; food analysis; blood;
 KW environmental analysis; plant protection; veterinary medicine;
 KW human immune deficiency virus; hepatitis B; hepatitis C; Chlamydia;
 KW screening; PCR primer; detection; probe; ss.
 XX
 OS Synthetic.
 OS
 FH Key Location/Qualifiers
 FT modified_base 1 /*tag- a
 FT /note- "5'-end labelled with ruthenium"
 XX
 PN DE19748690-A1.
 XX
 PD 06-MAY-1999.
 XX
 PE 04-NOV-1997; 97DE-1048690.
 XX
 PR 04-NOV-1997; 97DE-1048690.
 XX
 PA (HOFF) ROCHE DIAGNOSTICS GMBH.
 XX
 DR WPI; 1999-278780/24.
 XX
 PT Detecting nucleic acid by generating short amplicons and probing
 PT e.g. for diagnosis, food and environmental analysis and plant
 PT protection
 XX
 PS Example 1; Page 18; 22pp; German.
 XX
 CC This invention describes a method for the detection of nucleic acid
 CC which comprises amplification and reaction of the amplicon with a probe.
 CC The method is used to detect nucleic acid e.g. for medical or forensic
 CC diagnosis, in food and environmental analysis, in plant protection and
 CC veterinary medicine, e.g. for detecting human immune deficiency virus,
 CC hepatitis B or C viruses, or Chlamydia, in blood screening. The method
 CC provides target-dependent, exponential amplification for highly specific
 CC and sensitive, reproducible and quantitative detection of one or more
 CC nucleic acids (single or double stranded). The design of primers and
 CC probes is sufficiently flexible to allow many nucleic acids to be
 CC detected in a standardized reaction format using partly the same primers
 CC and probes. Only small amplicons are produced (requiring short
 CC amplification cycles), there is no competition/displacement between the
 CC short counter-strand of the amplicon and the detection probe, and


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XX 26-FEB-1994.
PD
XX 23-AUG-1993; 93CA-2104649.
XX
XX 25-AUG-1992; 92JP-0248796.
PR 03-MAR-1993; 93JP-0042736.
XX
XX (SEKI/) SEKI M.
XX
XX Honda Y, Seki M, Yamada E;
PI
XX WPI; 1994-151836/19.
DR
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT virus genome - are useful as antiviral agents
XX
XX Claim 5; Page 163; 262pp; English.
PS
XX This oligonucleotide is an example of a preferred antisense compound
CC 1.e. it has a base sequence of 15-30 bases which is included
CC within the 49 bases from G at position 127 to C at position 175 of
CC AA064913 and which contains at least 7 bases from C at position 147
CC to C at position 153. The antisense oligonucleotide is useful for
CC inhibiting translation of HCV genes.
CC
XX Sequence 16 BP; 2 A; 2 C; 10 G; 2 T; 0 other;
SQ
XX
XX Query Match 100.0%; Score 12; DB 15; Length 16;
XX Best Local Similarity 83.3%; Pred. No. 1e+03; 0; Indels 0; Gaps 0;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCGCGAG 12
XX ||||:|||||
XX 5 ggggtcctcgag 16
Db
XX
XX RESULT 7
XX AA065125
XX ID AA065125 standard; DNA; 16 BP.
XX
XX AA065125;
AC
XX 21-DEC-1994 (first entry)
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
DE
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW therapy; inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS
XX CA2104649-A.
PN
XX 26-FEB-1994.
PD
XX 23-AUG-1993; 93CA-2104649.
PF
XX 25-AUG-1992; 92JP-0248796.
PR 03-MAR-1993; 93JP-0042736.
XX
XX (SEKI/) SEKI M.
PA
XX Honda Y, Seki M, Yamada E;
PI
XX WPI; 1994-151836/19.
DR
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT virus genome - are useful as antiviral agents
XX
XX Claim 5; Page 156; 262pp; English.
XX

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CC This oligonucleotide is an example of a preferred antisense compound
CC 1.e. it has a base sequence of 15-30 bases which is included
CC within the 49 bases from G at position 127 to C at position 175 of
CC AA064913 and which contains at least 7 bases from C at position 147
CC to C at position 153. The antisense oligonucleotide is useful for
CC inhibiting translation of HCV genes.
CC
XX Sequence 16 BP; 1 A; 2 C; 11 G; 2 T; 0 other;
SQ
XX
XX Query Match 100.0%; Score 12; DB 15; Length 16;
XX Best Local Similarity 83.3%; Pred. No. 1e+03; 0; Indels 0; Gaps 0;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCGCGAG 12
XX ||||:|||||
XX 4 ggggtcctcgag 15
Db
XX
XX RESULT 8
XX AAT90622
XX ID AAT90622 standard; RNA; 16 BP.
XX
XX AAT90622;
AC
XX 07-APR-1998 (first entry)
XX
XX Hepatitis C virus recognition sequence 32 for ribozyme cleavage.
DE
XX
XX Recognition sequence; HCV; ribozyme; 5' untranslated region;
KW nucleocapsid coding region; hairpin ribozyme; RNA cleavage;
KW treatment; HCV infection; HCV contamination; ss.
XX
XX Hepatitis C virus.
OS
XX
XX Key Location/Qualifiers
XX misc_feature 1..4
XX /*tag- a
XX /note- "complementary to the CNR2 ribozyme"
XX misc_feature 6
XX /*tag- b
XX /note- "cleavage site corresponding to position 120
XX of the (-) strand, counting from 3' end"
XX misc_feature 9..16
XX /*tag- c
XX /note- "complementary to the CNR2 ribozyme"
XX
XX WO9732018-A2.
PN
XX 04-SEP-1997.
PD
XX 27-FEB-1997; 97MO-US03304.
PF
XX 29-FEB-1996; 96US-0608862.
PR
XX (IMMU-) IMMUSOL INC.
PA
XX Barber JR, Tritz R, Welch PJ, Yel S, Yu M;
PI
XX WPI; 1997-470461/43.
DR
XX
XX Ribozyme(s) directed against hepatitis C virus - for prevention and
PT treatment of viral infection, and detection of HCV contamination of
PT blood
XX
XX Example 1; Page 17; 98pp; English.
PS
XX AAT90621-650 represent recognition sequences found in the positive (-)
XX strand of the Hepatitis C virus (HCV) RNA. The sequences are recognised
XX by novel ribozymes which inhibit replication, infectivity or gene
XX expression of HCV. The present sequence is located within the 5' UTR.
XX Hairpin ribozymes of the present invention were designed based on
XX sequences adjacent to the GUC sequence recognition feature. The
CC

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DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW therapy; inhibition; viral protein precursor; ss.
XX Synthetic.
OS
XX CA2104649-A.
XX
XX 26-FEB-1994.
XX
XX 23-AUG-1993; 93CA-2104649.
XX
XX 25-AUG-1992; 93JP-0248796.
XX
XX 03-MAR-1993; 93JP-0042736.
XX
XX (SEKI/) SEKI M.
XX
XX Honda Y, Seki M, Yamada E;
XX
XX WPI; 1994-151836/19.
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
XX virus genome - are useful as antiviral agents
XX
XX Claim 5; Page 157; 262pp; English.
XX
XX This oligonucleotide is an example of a preferred antisense compound
XX i.e. it has a base sequence of 15-30 bases which is included
XX within the 49 bases from G at position 127 to C at position 175 of
XX AA065143 and which contains at least 7 bases from C at position 147
XX to C at position 153. The antisense oligonucleotide is useful for
XX inhibiting translation of HCV genes.
XX
XX Sequence 17 BP; 2 A; 2 C; 11 G; 2 T; 0 other;
SQ

Query Match 100.0%; Score 12; DB 15; Length 17;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCUGGAG 12
DB 5 999gtccctgag 16

RESULT 12
AA065111
ID AA065111 standard; DNA; 17 BP.
XX
XX AA065111;
XX
XX 21-DEC-1994 (first entry)
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW therapy; inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS
XX CA2104649-A.
XX
XX 26-FEB-1994.
XX
XX 23-AUG-1993; 93CA-2104649.
XX
XX 25-AUG-1992; 93JP-0248796.
XX
XX 03-MAR-1993; 93JP-0042736.
XX
XX (SEKI/) SEKI M.
XX
XX Honda Y, Seki M, Yamada E;
XX
XX
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XX
XX WPI; 1994-151836/19.
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
XX virus genome - are useful as antiviral agents
XX
XX Claim 5; Page 150; 262pp; English.
XX
XX This oligonucleotide is an example of a preferred antisense compound
XX i.e. it has a base sequence of 15-30 bases which is included
XX within the 49 bases from G at position 127 to C at position 175 of
XX AA064913 and which contains at least 7 bases from C at position 147
XX to C at position 153. The antisense oligonucleotide is useful for
XX inhibiting translation of HCV genes.
XX
XX Sequence 17 BP; 1 A; 3 C; 11 G; 2 T; 0 other;
SQ

Query Match 100.0%; Score 12; DB 15; Length 17;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCUGGAG 12
DB 4 999gtccctgag 15

RESULT 13
AA065143
ID AA065143 standard; DNA; 18 BP.
XX
XX AA065143;
XX
XX 21-DEC-1994 (first entry)
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW therapy; inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS
XX CA2104649-A.
XX
XX 26-FEB-1994.
XX
XX 23-AUG-1993; 93CA-2104649.
XX
XX 25-AUG-1992; 93JP-0248796.
XX
XX 03-MAR-1993; 93JP-0042736.
XX
XX (SEKI/) SEKI M.
XX
XX Honda Y, Seki M, Yamada E;
XX
XX WPI; 1994-151836/19.
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
XX virus genome - are useful as antiviral agents
XX
XX Claim 5; Page 164; 262pp; English.
XX
XX This oligonucleotide is an example of a preferred antisense compound
XX i.e. it has a base sequence of 15-30 bases which is included
XX within the 49 bases from G at position 127 to C at position 175 of
XX AA064913 and which contains at least 7 bases from C at position 147
XX to C at position 153. The antisense oligonucleotide is useful for
XX inhibiting translation of HCV genes.
XX
XX Sequence 18 BP; 2 A; 2 C; 12 G; 2 T; 0 other;
SQ

Query Match 100.0%; Score 12; DB 15; Length 18;
XX
```

Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGAG 12
||||:|||||
Db 7 999gtcctgag 18

RESULT 14

AA065127 standard; DNA; 18 BP.

AA065127;

21-DEC-1994 (first entry)

DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.

KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;

XX therapy; inhibition; viral protein precursor; ss.

OS Synthetic.

PN CA2104649-A.

PD 26-FEB-1994.

PF 23-AUG-1993; 93CA-2104649.

PR 25-AUG-1992; 92JP-0248796.

PR 03-MAR-1993; 93JP-0042736.

PA (SEKI/) SEKI M.

PI Honda Y, Seki M, Yamada E;

DR WPI; 1994-151836/19.

PT Anti-sense oligo:nucleotide(s) complementary to the hepatitis C

XX virus genome - are useful as antiviral agents

PS Claim 5; Page 157; 262pp; English.

CC This oligonucleotide is an example of a preferred antisense compound
i.e. it has a base sequence of 15-30 bases which is included
within the 49 bases from G at position 127 to C at position 175 of
CC AA064913 and which contains at least 7 bases from C at position 147
to C at position 153. The antisense oligonucleotide is useful for
inhibiting translation of HCV genes.

SQ Sequence 18 BP; 2 A; 2 C; 12 G; 2 T; 0 other;

Query Match 100.0%; Score 12; DB 15; Length 18;

Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGAG 12
||||:|||||
Db 6 999gtcctgag 17

RESULT 15

AA065112 standard; DNA; 18 BP.

AA065112;

21-DEC-1994 (first entry)

DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.

XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;

KM therapy; inhibition; viral protein precursor; ss.

OS Synthetic.

PN CA2104649-A.

PD 26-FEB-1994.

PF 23-AUG-1993; 93CA-2104649.

PR 25-AUG-1992; 92JP-0248796.

PR 03-MAR-1993; 93JP-0042736.

PA (SEKI/) SEKI M.

PI Honda Y, Seki M, Yamada E;

DR WPI; 1994-151836/19.

PT Anti-sense oligo:nucleotide(s) complementary to the hepatitis C

XX virus genome - are useful as antiviral agents

PS Claim 5; Page 151; 262pp; English.

CC This oligonucleotide is an example of a preferred antisense compound
i.e. it has a base sequence of 15-30 bases which is included
within the 49 bases from G at position 127 to C at position 175 of
CC AA064913 and which contains at least 7 bases from C at position 147
to C at position 153. The antisense oligonucleotide is useful for
inhibiting translation of HCV genes.

SQ Sequence 18 BP; 2 A; 3 C; 11 G; 2 T; 0 other;

Query Match 100.0%; Score 12; DB 15; Length 18;

Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGAG 12
||||:|||||
Db 5 999gtcctgag 16

Search completed: August 8, 2001, 16:06:02
Job time: 3966 sec

CNA

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 8, 2001, 16:01:27 ; Search time 1583.8 Seconds
(without alignments)
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Title: US-08-887-505-122

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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98:	em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	20	100.0	27	9 AR106359	AR106359 Sequence
2	20	100.0	33	9 AR004396	AR004396 Sequence
3	20	100.0	33	9 AR064935	AR064935 Sequence
4	20	100.0	33	9 AR097188	AR097188 Sequence
5	20	100.0	33	10 182871	182871 Sequence 50
6	20	100.0	46	10 144581	144581 Sequence 10
7	20	100.0	46	10 170986	170986 Sequence 10
c 8	20	100.0	139	58 AF282631	AF282631 Hepatitis

C 9 20 100.0 139 58 AF282632
C 10 20 100.0 139 58 AF282633
C 11 20 100.0 139 58 AF282634
C 12 20 100.0 139 58 AF282635
C 13 20 100.0 139 58 AF282637
C 14 20 100.0 139 58 AF282638
C 15 20 100.0 139 58 AF282639
C 16 20 100.0 139 58 AF282640
C 17 20 100.0 139 58 AF282641
C 18 20 100.0 139 58 AF282642
C 19 20 100.0 139 58 AF282643
C 20 20 100.0 139 58 AF282644
C 21 20 100.0 139 58 AF282645
C 22 20 100.0 139 58 AF282646
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C 24 20 100.0 139 58 AY003922
C 25 20 100.0 139 58 AY003923
C 26 20 100.0 139 58 AY003924
C 27 20 100.0 139 58 AY003925
C 28 20 100.0 139 58 AY003928
C 29 20 100.0 139 58 AY003929
C 30 20 100.0 139 58 AY003930
C 31 20 100.0 139 58 AY003932
C 32 20 100.0 139 58 AY003933
C 33 20 100.0 139 58 AY003934
C 34 20 100.0 139 58 AY003935
C 35 20 100.0 139 58 AY003936
C 36 20 100.0 139 58 AY003937
C 37 20 100.0 139 58 AY003938
C 38 20 100.0 139 58 AY003939
C 39 20 100.0 139 58 AY003940
C 40 20 100.0 139 58 AY003941
C 41 20 100.0 139 58 AY003942
C 42 20 100.0 139 58 AY003943
C 43 20 100.0 139 58 AY003944
C 44 20 100.0 139 58 AY003945
C 45 20 100.0 139 58 AY004013

ALIGNMENTS

RESULT 1
LOCUS AR106359/c 27 bp DNA PAT 14-FEB-2001
DEFINITION Sequence 21 from patent US 6107028.
ACCESSION AR106359
VERSION AR106359.1 GI:12820889
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 27)
AUTHORS Kay/M.A. and Lieber/A.
TITLE Ribozymes for treating hepatitis C
JOURNAL Patent: US 6107028-A 21 22-AUG-2000;
FEATURES
source Location/Qualifiers
1..27
/organism="unknown"

BASE COUNT 6 a 4 c 12 g 5 t
ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 27;
Best Local Similarity 80.0%; Pred. No. 0.44;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 UUGCGAGCCACACACACAC 20

Db 24 TTTCGAGCCACACACACAC 5

RESULT 2

AR004396
LOCUS AR004396 33 bp DNA PAT 04-DEC-1998
DEFINITION Sequence 50 from patent US 5747244.
ACCESSION AR004396
VERSION AR004396.1 GI:3965275
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 33)
AUTHORS Sheridan,P., Chang,C., Running,J. and Urdea,M.S.
TITLE Nucleic acid probes immobilized on polystyrene surfaces
JOURNAL Patent: US 5747244-A 50 05-MAY-1998;
FEATURES
source Location/Qualifiers
1..33
/organism="unknown"

BASE COUNT 8 a 13 c 6 g 6 t
ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 33;
Best Local Similarity 80.0%; Pred. No. 0.44;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 UUGCGAGCCACACACACAC 20
Db 10 TTTCGAGCCACACACACAC 29

RESULT 3
LOCUS AR064935 33 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 60 from patent US 5849481.
ACCESSION AR064935
VERSION AR064935.1 GI:5995151
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 33)
AUTHORS Urdea,M.S., Horn,T., Chang,C., Warner,B. and Fultz,T.J.
TITLE Nucleic acid hybridization assays employing large comb-type branched polynucleotides
JOURNAL Patent: US 5849481-A 60 15-DEC-1998;
FEATURES
source Location/Qualifiers
1..33
/organism="unknown"

BASE COUNT 8 a 13 c 6 g 6 t
ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 33;
Best Local Similarity 80.0%; Pred. No. 0.44;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 UUGCGAGCCACACACACAC 20

Db 10 TTTCGAGCCACACACACAC 29

RESULT 4
LOCUS AR097188 33 bp DNA PAT 14-FEB-2001
DEFINITION Sequence 126 from patent US 6071693.
ACCESSION AR097188
VERSION AR097188.1 GI:12805918
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 33)
AUTHORS Cha,T., Beall,E., Irvine,B., Kolberg,J. and Urdea,M.S.
TITLE HCV genomic sequences for diagnostics and therapeutics

JOURNAL Patent: US 6071693-A 126 06-JUN-2000;
FEATURES Location/Qualifiers
source 1..33
/organism="unknown"
BASE COUNT 8 a 13 c 6 g 6 t
ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 33;
Best Local Similarity 80.0%; Pred. No. 0.44;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 UUCGCGACCCACACUACUC 20
Db 10 TTCCGACCCACACACTACTC 29

RESULT 5
LOCUS 182871 33 bp DNA PAT 10-JUN-1998
DEFINITION Sequence 50 from patent US 5712383.
ACCESSION 182871
VERSION 182871.1 GI:3211168
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 33)
AUTHORS Sheridan,P., Chang,C., Running,J. and Urdea,M.S.
TITLE Processes for immobilizing nucleic acid probes on polystyrene
surfaces
JOURNAL Patent: US 5712383-A 50 27-JAN-1998;
FEATURES Location/Qualifiers
source 1..33
/organism="unknown"

BASE COUNT 8 a 13 c 6 g 6 t
ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 33;
Best Local Similarity 80.0%; Pred. No. 0.44;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 UUCGCGACCCACACUACUC 20
Db 10 TTCCGACCCACACACTACTC 29

RESULT 6
LOCUS 144581 46 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 10 from patent US 5635352.
ACCESSION 144581
VERSION 144581.1 GI:2469294
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 46)
AUTHORS Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
TITLE Solution phase nucleic acid sandwich assays having reduced
background noise
JOURNAL Patent: US 5635352-A 10 03-JUN-1997;
FEATURES Location/Qualifiers
source 1..46
/organism="unknown"

BASE COUNT 9 a 17 c 11 g 9 t
ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 46;
Best Local Similarity 80.0%; Pred. No. 0.45;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 UUCGCGACCCACACUACUC 20
Db 10 TTCCGACCCACACACTACTC 29

RESULT 7
LOCUS 170986 46 bp DNA PAT 03-APR-1998
DEFINITION Sequence 10 from patent US 5681697.
ACCESSION 170986
VERSION 170986.1 GI:3007121
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 46)
AUTHORS Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
TITLE Solution phase nucleic acid sandwich assays having reduced
background noise and kits therefor
JOURNAL Patent: US 5681697-A 10 28-OCT-1997;
FEATURES Location/Qualifiers
source 1..46
/organism="unknown"

BASE COUNT 9 a 17 c 11 g 9 t
ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 46;
Best Local Similarity 80.0%; Pred. No. 0.45;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 UUCGCGACCCACACUACUC 20
Db 10 TTCCGACCCACACACTACTC 29

RESULT 8
LOCUS AF282631 139 bp RNA VRL 01-MAR-2001
DEFINITION Hepatitis C virus isolate H069 clone 1 5' non-coding region
sequence.
ACCESSION AF282631
VERSION AF282631.1 GI:10764494
KEYWORDS
SOURCE Hepatitis C virus.
ORGANISM Hepatitis C virus.
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.

REFERENCE 1 (bases 1 to 139)
AUTHORS Harris,K.A. and Teo,C.G.
TITLE Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
Gradient Gel Electrophoresis
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
PUBMED 11139197

REFERENCE 2 (bases 1 to 139)
AUTHORS Harris,K.A. and Teo,C.G.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
Central Public Health Laboratory, 61 Colindale Avenue, London NW9
5HT, UK

FEATURES Location/Qualifiers
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/isolate="H069"
/db_xref="taxon:11103"
/clone="1"

misc_feature 1..139
BASE COUNT 28 a 36 c 43 g 32 t
ORIGIN

Query Match 100.0%; Score 20; DB 58; Length 139;
 Best Local Similarity 80.0%; Pred. No. 0.46;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 UUCGCGACCCACACUACUC 20
 :::::::::::::::::::::
 Db 116 TTCGCGACCCACACUACUC 97

RESULT 9
 AF282632/C 139 bp RNA VRL 01-MAR-2001
 LOCUS AF282632
 DEFINITION Hepatitis C virus isolate H069 clone II 5' non-coding region
 sequence.
 ACCESSION AF282632
 VERSION AF282632.1 GI:10764495
 KEYWORDS
 SOURCE Hepatitis C virus.
 ORGANISM Hepatitis C virus.
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Hepacivirus.

REFERENCE 1 (bases 1 to 139)
 AUTHORS Harris, K.A. and Teo, C.G.
 TITLE Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
 Gradient Gel Electrophoresis
 JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
 PUBMED 11139197

REFERENCE 2 (bases 1 to 139)
 AUTHORS Harris, K.A. and Teo, C.G.
 TITLE Direct Submission
 JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
 Central Public Health Laboratory, 61 Colindale Avenue, London NW9
 5HT, UK

FEATURES
 source 1..139 Location/Qualifiers
 /organism="Hepatitis C virus"
 /isolate="H069"
 /db_xref="taxon:11103"
 /clone="II"
 misc_feature 1..139
 /note="5' non-coding region"
 BASE COUNT 28 a 36 c 42 g 33 t
 ORIGIN

Query Match 100.0%; Score 20; DB 58; Length 139;
 Best Local Similarity 80.0%; Pred. No. 0.46;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 UUCGCGACCCACACUACUC 20
 :::::::::::::::::::::
 Db 116 TTCGCGACCCACACUACUC 97

RESULT 10
 AF282633/C 139 bp RNA VRL 01-MAR-2001
 LOCUS AF282633
 DEFINITION Hepatitis C virus isolate H071 clone I 5' non-coding region
 sequence.
 ACCESSION AF282633
 VERSION AF282633.1 GI:10764496
 KEYWORDS
 SOURCE Hepatitis C virus.
 ORGANISM Hepatitis C virus.
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Hepacivirus.

REFERENCE 1 (bases 1 to 139)
 AUTHORS Harris, K.A. and Teo, C.G.
 TITLE Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
 Gradient Gel Electrophoresis
 JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
 PUBMED 11139197
 REFERENCE 2 (bases 1 to 139)

AUTHORS Harris, K.A. and Teo, C.G.
 TITLE Direct Submission
 JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
 Central Public Health Laboratory, 61 Colindale Avenue, London NW9
 5HT, UK

FEATURES
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 /isolate="H071"
 /db_xref="taxon:11103"
 /clone="I"
 misc_feature 1..139
 /note="5' non-coding region"
 BASE COUNT 27 a 37 c 43 g 32 t
 ORIGIN

Query Match 100.0%; Score 20; DB 58; Length 139;
 Best Local Similarity 80.0%; Pred. No. 0.46;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 UUCGCGACCCACACUACUC 20
 :::::::::::::::::::::
 Db 116 TTCGCGACCCACACUACUC 97

RESULT 11
 AF282634/C 139 bp RNA VRL 01-MAR-2001
 LOCUS AF282634
 DEFINITION Hepatitis C virus isolate H071 clone II 5' non-coding region
 sequence.
 ACCESSION AF282634
 VERSION AF282634.1 GI:10764497
 KEYWORDS
 SOURCE Hepatitis C virus.
 ORGANISM Hepatitis C virus.
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Hepacivirus.

REFERENCE 1 (bases 1 to 139)
 AUTHORS Harris, K.A. and Teo, C.G.
 TITLE Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
 Gradient Gel Electrophoresis
 JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
 PUBMED 11139197

REFERENCE 2 (bases 1 to 139)
 AUTHORS Harris, K.A. and Teo, C.G.
 TITLE Direct Submission
 JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
 Central Public Health Laboratory, 61 Colindale Avenue, London NW9
 5HT, UK

FEATURES
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 /db_xref="taxon:11103"
 /clone="II"
 misc_feature 1..139
 /note="5' non-coding region"
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 ORIGIN

Query Match 100.0%; Score 20; DB 58; Length 139;
 Best Local Similarity 80.0%; Pred. No. 0.46;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 UUCGCGACCCACACUACUC 20
 :::::::::::::::::::::
 Db 116 TTCGCGACCCACACUACUC 97

RESULT 12
 AF282635/C

LOCUS AF282635 139 bp RNA VRL 01-MAR-2001
DEFINITION Hepatitis C virus isolate H075 clone I 5' non-coding region
sequence.
AF282635
ACCESSION AF282635
VERSION AF282635.1 GI:10764498
KEYWORDS Hepatitis C virus.
SOURCE Hepatitis C virus.
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 139)
AUTHORS Harris,K.A. and Teo,C.G.
TITLE Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
Gradient Gel Electrophoresis
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
PUBMED 11139197
REFERENCE 2 (bases 1 to 139)
AUTHORS Harris,K.A. and Teo,C.G.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
Central Public Health Laboratory, 61 Colindale Avenue, London NW9
5HT, UK
FEATURES
source Location/Qualifiers
1.139
/organism="Hepatitis C virus"
/isolate="H075"
/db_xref="taxon:11103"
/clone="I"
misc_feature 1.139
/note="5' non-coding region"
BASE COUNT 26 a 37 c 44 g 32 t
ORIGIN
Query Match 100.0%; Score 20; DB 58; Length 139;
Best Local Similarity 80.0%; Pred. No. 0.46;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
OY 1 UUGCGAGCCAGACUACUC 20
Db 116 TTCGCGACCCACACTACTC 97
RESULT 13
AF282637/c 139 bp RNA VRL 01-MAR-2001
LOCUS Hepatitis C virus isolate H075 clone III 5' non-coding region
sequence.
AF282637
ACCESSION AF282637.1 GI:10764500
VERSION AF282637.1
KEYWORDS Hepatitis C virus.
SOURCE Hepatitis C virus.
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 139)
AUTHORS Harris,K.A. and Teo,C.G.
TITLE Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
Gradient Gel Electrophoresis
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
PUBMED 11139197
REFERENCE 2 (bases 1 to 139)
AUTHORS Harris,K.A. and Teo,C.G.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
Central Public Health Laboratory, 61 Colindale Avenue, London NW9
5HT, UK
FEATURES
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1.139
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/isolate="H075"
/db_xref="taxon:11103"
/clone="III"
misc_feature 1.139
/note="5' non-coding region"
BASE COUNT 26 a 36 c 44 g 33 t
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Best Local Similarity 80.0%; Pred. No. 0.46;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
OY 1 UUGCGAGCCAGACUACUC 20
Db 116 TTCGCGACCCACACTACTC 97
RESULT 15
AF282639/c 139 bp RNA VRL 01-MAR-2001
LOCUS Hepatitis C virus isolate H858 clone I 5' non-coding region
sequence.
AF282639
ACCESSION AF282639.1 GI:10764502
VERSION AF282639.1
KEYWORDS Hepatitis C virus.
SOURCE Hepatitis C virus.
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 139)

misc_feature 1.139
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BASE COUNT 26 a 36 c 44 g 33 t
ORIGIN
Query Match 100.0%; Score 20; DB 58; Length 139;
Best Local Similarity 80.0%; Pred. No. 0.46;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
OY 1 UUGCGAGCCAGACUACUC 20
Db 116 TTCGCGACCCACACTACTC 97
RESULT 14
AF282638/c 139 bp RNA VRL 01-MAR-2001
LOCUS Hepatitis C virus isolate H075 clone IV 5' non-coding region
sequence.
AF282638
ACCESSION AF282638.1 GI:10764501
VERSION AF282638.1
KEYWORDS Hepatitis C virus.
SOURCE Hepatitis C virus.
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 139)
AUTHORS Harris,K.A. and Teo,C.G.
TITLE Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
Gradient Gel Electrophoresis
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
PUBMED 11139197
REFERENCE 2 (bases 1 to 139)
AUTHORS Harris,K.A. and Teo,C.G.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
Central Public Health Laboratory, 61 Colindale Avenue, London NW9
5HT, UK
FEATURES
source Location/Qualifiers
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/isolate="H075"
/db_xref="taxon:11103"
/clone="IV"
misc_feature 1.139
/note="5' non-coding region"
BASE COUNT 26 a 36 c 44 g 33 t
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Best Local Similarity 80.0%; Pred. No. 0.46;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
OY 1 UUGCGAGCCAGACUACUC 20
Db 116 TTCGCGACCCACACTACTC 97
RESULT 15
AF282639/c 139 bp RNA VRL 01-MAR-2001
LOCUS Hepatitis C virus isolate H858 clone I 5' non-coding region
sequence.
AF282639
ACCESSION AF282639.1 GI:10764502
VERSION AF282639.1
KEYWORDS Hepatitis C virus.
SOURCE Hepatitis C virus.
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 139)

AUTHORS Harris, K.A. and Teo, C.G.
TITLE Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
JOURNAL Gradient Gel Electrophoresis
PUBMED Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
11139197
REFERENCE 2 (bases 1 to 139)
AUTHORS Harris, K.A. and Teo, C.G.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
Central Public Health Laboratory, 61 Colindale Avenue, London NW9
5HT, UK

FEATURES
source Location/Qualifiers
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misc_feature 1.139
BASE COUNT 26 a 37 c 44 g 32 t
ORIGIN

Query Match 100.0%; Score 20; DB 58; Length 139;
Best Local Similarity 80.0%; Pred. No. 0.46;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 UUUGCGAGCCCAACACACUACUC 20
:::|||||
DB 116 TTGCGAGCCCAACACACTACTC 97

Search completed: August 8, 2001, 16:01:28
Job time: 5802 sec

CC specificity is high because the relative proportion of the internal
 CC deletion region is increased with respect to the total amplicon length,
 CC allowing better differentiation between (viral) subtypes. Also short
 CC amplicons are less likely to undergo non-specific hybridization, so
 CC background is low, and short RNA sequences are more stable, with reduced
 CC tendency to form secondary structures. AAX23968-69 and AAX24035-37 are
 CC PCR primers and probes used in the method of the invention.

CC Sequence 12 BP; 2 A; 7 C; 2 G; 1 T; 0 other;

Query Match

Best Local Similarity 100.0%; Score 12; DB 20; Length 12;
 Pred. No. 1e+03;
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGCCUGGAG 12
 ||||:||||
 DB 12 GGGGCTCTGGAG 1

RESULT 4

AA070177/c
 ID AA070177 standard; RNA; 14 BP.

AC AA070177;

DE 04-OCT-1994 (first entry)

DE Hepatitis C virus 5'-UTR antisense oligonucleotide target (A).

KW Hepatitis C virus; HCV; non-A, non-B hepatitis virus; NANBHV;
 KW antisense oligonucleotide; translation inhibition; therapy;

KW 5'-untranslated region; ss.

XX Hepatitis C Virus.

OS MO9405813-A.

XX 17-MAR-1994.

PF 10-SEP-1993; 93MO-JP01293.

PR 10-SEP-1992; 92US-0945289.

PR 14-APR-1993; 93JP-0087195.

XX (KAGA) CEMO SERO THERAPEUTIC RES INST.

PA (ISIS-) ISIS PHARM INC.

PI Anderson KP, Eto T, Furukawa S, Hamada F, Hanecak RC;
 PI Hoshiko K, Nakatani H, Nishihara T, Nozaki C;

DR WPI; 1994-101217/12.

PT Anti-sense oligo:nucleotide(s) complementary to hepatitis C viral
 PT genome - useful for inhibiting HCV replication, to treat related
 PT diseases

XX Claim 16; Page 71; 91pp; English.

XX Oligonucleotides which are complementary to part of the hepatitis
 CC C virus genomic or messenger RNA are claimed. AA070177 is a preferred
 CC target sequence which is present in the 5'-UTR of the HCV genome.

XX Sequence 14 BP; 2 A; 8 C; 3 G; 1 U; 0 other;

XX Query Match

Best Local Similarity 100.0%; Score 12; DB 15; Length 14;
 Pred. No. 1e+03;
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGCCUGGAG 12
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XX 1 GGGGCCUGGAG 12
 ||||:||||

DB 14 GGGGCTCTGGAG 3

RESULT 5

AA065140
 ID AA065140 standard; DNA; 15 BP.

AC AA065140;

DE 21-DEC-1994 (first entry)

DE Antisense oligonucleotide complementary to Hepatitis C virus genome.

KW Hepatitis C virus; Non-A, non-B hepatitis virus; HCV; antisense;
 KW therapy; inhibition; viral protein precursor; ss.

XX Synthetic.

OS CA2104649-A.

PN 26-FEB-1994.

PF 23-AUG-1993; 93CA-2104649.

PR 25-AUG-1992; 92JP-0248796.

PR 03-MAR-1993; 93JP-0042736.

XX (SEKI/) SEKI M.

PI Honda Y, Seki M, Yamada E;

DR WPI; 1994-151836/19.

PT Anti-sense oligo:nucleotide(s) complementary to the hepatitis C
 PT virus genome - are useful as antiviral agents

XX Claim 5; Page 163; 262pp; English.

XX This oligonucleotide is an example of a preferred antisense compound
 CC i.e. it has a base sequence of 15-30 bases which is included
 CC within the 49 bases from G at position 127 to C at position 175 of
 CC AA064913 and which contains at least 7 bases from C at position 147
 CC to C at position 153. The antisense oligonucleotide is useful for
 CC inhibiting translation of HCV genes.

XX Sequence 15 BP; 1 A; 2 C; 10 G; 2 T; 0 other;

XX Query Match

Best Local Similarity 100.0%; Score 12; DB 15; Length 15;
 Pred. No. 1e+03;
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGCCUGGAG 12
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DB 4 GGGGCTCTGGAG 15

XX 1 GGGGCCUGGAG 12
 ||||:||||

XX 4 GGGGCTCTGGAG 15

XX RESULT 6

AA065141
 ID AA065141 standard; DNA; 16 BP.

AC AA065141;

DE 21-DEC-1994 (first entry)

DE Antisense oligonucleotide complementary to Hepatitis C virus genome.

KW Hepatitis C virus; Non-A, non-B hepatitis virus; HCV; antisense;
 KW therapy; inhibition; viral protein precursor; ss.

XX Synthetic.

OS CA2104649-A.

PN CA2104649-A.

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c 9 20 100.0 139 58 AF282632 Hepatitis
c 10 20 100.0 139 58 AF282633 Hepatitis
c 11 20 100.0 139 58 AF282634 Hepatitis
c 12 20 100.0 139 58 AF282635 Hepatitis
c 13 20 100.0 139 58 AF282636 Hepatitis
c 14 20 100.0 139 58 AF282637 Hepatitis
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c 16 20 100.0 139 58 AF282639 Hepatitis
c 17 20 100.0 139 58 AF282640 Hepatitis
c 18 20 100.0 139 58 AF282641 Hepatitis
c 19 20 100.0 139 58 AF282642 Hepatitis
c 20 20 100.0 139 58 AF282643 Hepatitis
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c 22 20 100.0 139 58 AF282645 Hepatitis
c 23 20 100.0 139 58 AF282646 Hepatitis
c 24 20 100.0 139 58 AF282647 Hepatitis
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c 26 20 100.0 139 58 AF282649 Hepatitis
c 27 20 100.0 139 58 AF282650 Hepatitis
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c 42 20 100.0 139 58 AF282665 Hepatitis
c 43 20 100.0 139 58 AF282666 Hepatitis
c 44 20 100.0 139 58 AF282667 Hepatitis
c 45 20 100.0 139 58 AF282668 Hepatitis

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ALIGNMENTS

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AF282632 Hepatitis
AF282633 Hepatitis
AF282634 Hepatitis
AF282635 Hepatitis
AF282636 Hepatitis
AF282637 Hepatitis
AF282638 Hepatitis
AF282639 Hepatitis
AF282640 Hepatitis
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AF282667 Hepatitis
AF282668 Hepatitis

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RESULT 1
LOCUS ARI06359/c 27 bp DNA
DEFINITION Sequence 21 from patent US 6107028.
ACCESSION ARI06359
VERSION ARI06359.1 GI:12820889
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 27)
AUTHORS Kay, M.A. and Lieber, A.
TITLES Ribozymes for treating hepatitis C
JOURNAL Patent: US 6107028-A 21 22 AUG-2000;
FEATURES
Location/Qualifiers
1..27
/organism="unknown"
BASE COUNT 6 a 4 c 12 g 5 t
ORIGIN

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Query Match 100.0%; Score 20; DB 9; Length 27;
Best Local Similarity 80.0%; Pred. No. 0.44;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
OY 1 UUCGGACCCCAACACUACUC 20
DB 24 TTCGGACCCCAACACTACTC 5

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AR004396
LOCUS AR004396 33 bp DNA
DEFINITION Sequence 50 from patent US 5747244.
ACCESSION AR004396
VERSION AR004396.1 GI:3965275
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Sheridan, P., Chang, C., Running, J. and Urdea, M.S.
TITLES Nucleic acid probes immobilized on polystyrene surfaces
JOURNAL Patent: US 5747244-A 50 05-MAY-1998;
FEATURES
Location/Qualifiers
1..33
/organism="unknown"
BASE COUNT 8 a 13 c 6 g 6 t
ORIGIN

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Query Match 100.0%; Score 20; DB 9; Length 33;
Best Local Similarity 80.0%; Pred. No. 0.44;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
OY 1 UUCGGACCCCAACACUACUC 20
DB 10 TTCGGACCCCAACACTACTC 29

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```

RESULT 3
LOCUS AR064935 33 bp DNA
DEFINITION Sequence 60 from patent US 5849481.
ACCESSION AR064935
VERSION AR064935.1 GI:5995151
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Urdea, M.S., Horn, T., Chang, C., Warner, B. and Fultz, T.J.
TITLES Nucleic acid hybridization assays employing large comp-type
branched polynucleotides
JOURNAL Patent: US 5849481-A 60 15-DEC-1998;
FEATURES
Location/Qualifiers
1..33
/organism="unknown"
BASE COUNT 8 a 13 c 6 g 6 t
ORIGIN

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Query Match 100.0%; Score 20; DB 9; Length 33;
Best Local Similarity 80.0%; Pred. No. 0.44;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
OY 1 UUCGGACCCCAACACUACUC 20
DB 10 TTCGGACCCCAACACTACTC 29

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RESULT 4
LOCUS AR097188 33 bp DNA
DEFINITION Sequence 126 from patent US 6071693.
ACCESSION AR097188
VERSION AR097188.1 GI:12805918
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Cha, T., Beall, E., Irvine, B., Kolberg, J. and Urdea, M.S.
TITLES HCV genomic sequences for diagnostics and therapeutics

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JOURNAL Patent: US 6071693-A 126 06-JUN-2000;
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BASE COUNT 8 a 13 c 6 g 6 t
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 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 UUCGCGACCCACACUACUC 20
 Db 10 TTCGCGACCCACACACTACTC 29

RESULT 5
 LOCUS 182871 33 bp DNA PAT 10-JUN-1998
 DEFINITION Sequence 50 from patent US 5712383.
 ACCESSION 182871
 VERSION 182871.1 GI:3211168
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 33)
 AUTHORS Sheridan,P., Chang,C., Running,J. and Urdea,M.S.
 TITLE Process for immobilizing nucleic acid probes on polystyrene surfaces
 JOURNAL Patent: US 5712383-A 50 27-JAN-1998;
 FEATURES Location/Qualifiers
 source 1..33
 /organism="unknown"

BASE COUNT 8 a 13 c 6 g 6 t
 ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 33;
 Best Local Similarity 80.0%; Pred. No. 0.44;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 UUCGCGACCCACACUACUC 20
 Db 10 TTCGCGACCCACACACTACTC 29

RESULT 6
 LOCUS 144581 46 bp DNA PAT 07-OCT-1997
 DEFINITION Sequence 10 from patent US 5635352.
 ACCESSION 144581
 VERSION 144581.1 GI:2469294
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 46)
 AUTHORS Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
 TITLE Solution phase nucleic acid sandwich assays having reduced background noise
 JOURNAL Patent: US 5635352-A 10 03-JUN-1997;
 FEATURES Location/Qualifiers
 source 1..46
 /organism="unknown"

BASE COUNT 9 a 17 c 11 g 9 t
 ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 46;
 Best Local Similarity 80.0%; Pred. No. 0.45;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 UUCGCGACCCACACUACUC 20
 Db 10 TTCGCGACCCACACACTACTC 29

RESULT 7
 LOCUS 170986 46 bp DNA PAT 03-APR-1998
 DEFINITION Sequence 10 from patent US 5681697.
 ACCESSION 170986
 VERSION 170986.1 GI:3007121
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 46)
 AUTHORS Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
 TITLE Solution phase nucleic acid sandwich assays having reduced background noise and kits therefor
 JOURNAL Patent: US 5681697-A 10 28-OCT-1997;
 FEATURES Location/Qualifiers
 source 1..46
 /organism="unknown"

BASE COUNT 9 a 17 c 11 g 9 t
 ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 46;
 Best Local Similarity 80.0%; Pred. No. 0.45;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 UUCGCGACCCACACUACUC 20
 Db 10 TTCGCGACCCACACACTACTC 29

RESULT 8
 LOCUS AF282631 139 bp RNA VRL 01-MAR-2001
 DEFINITION Hepatitis C virus isolate H069 clone I 5' non-coding region
 ACCESSION AF282631
 VERSION AF282631.1 GI:10764494
 KEYWORDS
 SOURCE Hepatitis C virus.
 ORGANISM Hepatitis C virus.
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1 (bases 1 to 139)
 AUTHORS Harris,K.A. and Teo,C.G.
 TITLE Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing Gradient Gel Electrophoresis
 JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
 PUBMED 11139197
 REFERENCE 2 (bases 1 to 139)
 AUTHORS Harris,K.A. and Teo,C.G.
 TITLE Direct Submission
 JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
 Central Public Health Laboratory, 61 Colindale Avenue, London NW9
 5HT, UK

FEATURES Location/Qualifiers
 source 1..139
 /organism="Hepatitis C virus"
 /isolate="H069"
 /db_xref="taxon:11103"
 /clone="I"

misc_feature 1..139
 /note="5' non-coding region"
 BASE COUNT 28 a 36 c 43 g 32 t
 ORIGIN